## APPENDIX A

1. A mutant mammalian G-protein coupled receptor having an amino acid sequence which differs from a wild type G protein-coupled receptor having a wild type amino acid sequence comprising an amino acid motif ($X_1X_2X_3X_4$) proximal to the carboxy terminal end of said wild type amino acid sequence, wherein:

$X_1$ denotes an amino acid residue at position 1 of said motif and is selected from the group consisting of Phe, Leu, Val, and Tyr;

$X_2$ denotes an amino acid residue at position 2 of said motif and is selected from the group consisting of Phe, Lys and Gln;

$X_3$ denotes an amino acid residue at position 3 of said motif and is selected from the group consisting of Leu, Arg, Glu, Asn, Gln, Ser, Ala, Leu ; and

$X_4$ denotes an amino acid residue at position 4 of said motif and is selected from the group consisting of Ala, Cys, Asp, Glu, Gly, Ser, Thr and Tyr; and

wherein said mutant receptor comprises a seventh transmembrane domain with a carboxy terminal end;

at least one point mutation at a position in said amino acid motif;

wherein upon interaction with a ligand to modulate a signal transduction pathway in a cell, a signal generated by said mutant receptor is greater than a signal generated upon interaction of said ligand with a wild type G protein-coupled receptor.

2. The receptor of claim 1, wherein said cell is a yeast cell.

3. The receptor of claim 2, wherein said receptor acts as a surrogate for an endogenous yeast pheromone receptor in a pheromone response pathway of said cell.

4. The receptor of claim 2, wherein said cell belongs to the species *Saccharomyces cerevisiae*.

5. The receptor of claim 1, wherein said cell is a mammalian cell.

6. The receptor of claim 1, wherein said receptor containing said amino acid motif with no point mutation thereon generates no detectable signal.

7. The receptor of claim 1, wherein said point mutation comprises mutagenization at position 4 of said amino acid motif to Arg or to Lys.

8. The receptor of claim 1, wherein said wild type G protein coupled receptor is IL8A receptor.

9. The receptor of claim 8, wherein said point mutation is selected from the group consisting of : Arg to Trp at position 73, Met to Ile at position 246; and Gly to Arg at position 320.

10. The receptor of claim 8, wherein said ligand is interleukin 8 (IL8) or melanoma growth-stimulating activity-alpha (MGSA/GROα).

11. The receptor of claim 1, wherein said wild type G protein coupled receptor is a human receptor.

12. The receptor of claim 11, wherein said wild type G protein coupled receptor is selected from the group consisting of human galanin-1 receptor, somatastatin receptor type I, somatastatin receptor type II, somatastatin receptor type III, and human nociceptin receptor.

13. The receptor of claim 12, wherein said wild type G protein coupled receptor is human galanin-1 receptor.

14. The receptor of claim 13, comprising an amino acid sequence LAYSNSSVNPIIYAFLSEN(FRKR)YKQV (SEQ ID NO:1) wherein said mutant amino acid motif within said sequence is (FRKR).

43. The receptor of claim 1, wherein said wild type G protein coupled receptor is a member of the rhodopsin family of receptors.

44. A mutant mammalian IL8A receptor having an amino acid sequence which differs from a wild type IL8A receptor having a wild type amino acid sequence comprising an amino acid motif ($X_1X_2X_3X_4$) proximal to the carboxy terminal end of said wild type amino acid sequence, wherein:

$X_1$ denotes an amino acid residue at position 1 of said motif and is selected from the group consisting of Phe, Leu, Val, and Tyr;

$X_2$ denotes an amino acid residue at position 2 of said motif and is selected from the group consisting of Phe, Lys and Gln;

$X_3$ denotes an amino acid residue at position 3 of said motif and is selected from the group consisting of Leu, Arg, Glu, Asn, Gln, Ser, Ala, Leu ; and

$X_4$ denotes an amino acid residue at position 4 of said motif and is selected from the group consisting of Ala, Cys, Asp, Glu, Gly, Ser, Thr and Tyr; and

wherein said mutant receptor comprises a seventh transmembrane domain with a carboxy terminal end; and

at least one point mutation at a position in said amino acid motif, wherein said point mutation is selected from the group consisting of: Arg to Trp at position 73, Met to Ile at position 246, and Gly to Arg at position 320, wherein upon interaction with a ligand to modulate a signal transduction pathway in a cell, a signal generated by said mutant receptor is greater than a signal generated upon interaction of said ligand with a wild type IL8A receptor.

45. The receptor of claim 44, wherein said cell is a yeast cell.

46. The receptor of claim 45, wherein said receptor acts as a surrogate for an endogenous yeast pheromone receptor in a pheromone response pathway of said cell.

47. The receptor of claim 45, wherein said cell belongs to the species *Saccharomyces cerevisiae*.

48. The receptor of claim 44, wherein said cell is a mammalian cell.

49. The receptor of claim 44, wherein said receptor containing said amino acid motif with no point mutation therein generates no detectable signal.

50. The receptor of claim 44, wherein said point mutation comprises mutagenization at position 4 of said amino acid motif to Arg or to Lys.

51. The receptor of claim 44, wherein said ligand is interleukin 8 (IL8) or melanoma growth-stimulating activity-alpha (MGSA/GROα).

52. A mutant galanin receptor-1 having an amino acid sequence which differs from a wild type galanin receptor-1 having a wild type amino acid sequence comprising an amino acid motif ($X_1X_2X_3X_4$) proximal to the carboxy terminal end of said wild type amino acid sequence, wherein:

$X_1$ denotes an amino acid residue at position 1 of said motif and is selected from the group consisting of Phe, Leu, Val, and Tyr;

$X_2$ denotes an amino acid residue at position 2 of said motif and is selected from the group consisting of Phe, Lys and Gln;

$X_3$ denotes an amino acid residue at position 3 of said motif and is selected from the group consisting of Leu, Arg, Glu, Asn, Gln, Ser, Ala, Leu ; and

$X_4$ denotes an amino acid residue at position 4 of said motif and is selected from the group consisting of Ala, Cys, Asp, Glu, Gly, Ser, Thr and Tyr; and

wherein said mutant receptor comprises a seventh transmembrane domain with a carboxy terminal end; and

at least one point mutation in said amino acid motif comprising Gly to Ala at position 320, wherein upon interaction with a ligand to modulate a signal

transduction pathway in a cell, a signal generated by said mutant receptor is greater than a signal generated upon interaction of said ligand with a wild type galanin receptor-1.

53. The amino acid motif of claim 52, wherein $X_1$ denotes an amino acid residue at position 1 of said motif and is Phe;

$X_2$ denotes an amino acid residue at position 2 of said motif and is selected from the group consisting of Arg;

$X_3$ denotes an amino acid residue at position 3 of said motif and is selected from the group consisting of Lys; and

$X_4$ denotes an amino acid residue at position 4 of said motif and is Ala, Cys, Asp, Glu, Gly, Ser, Thr and Tyr.

54. The receptor of claim 52 or 53, wherein said cell is a yeast cell.

55. The receptor of claim 54, wherein said receptor acts as a surrogate for an endogenous yeast pheromone receptor in a pheromone response pathway of said cell.

56. The receptor of claim 54, wherein said cell belongs to the species *Saccharomyces cerevisiae*.

57. The receptor of claim 52 or 53, wherein said cell is a mammalian cell.

58. The receptor of claim 52 or 53, wherein said receptor containing said amino acid motif with no point mutation therein generates no detectable signal.

59. The receptor of claim 52 or 53, wherein said receptor comprises mutagenization at position 4 of said amino acid motif to Arg or to Lys.